GenCore version 4.5 Copyright (c) 1993 - 2000 Comp Compugen Ltd.

OM nucleic - nucleic search, using sw model

Title: Perfect score: US-09-668-119-1 1740

Sequence: 1 atgaggaaagctggtgtggc.....cacattcgttccagccatga 1740

April 30, 2002, 19:51:03; Search time 2499.58 Seconds (without alignments)
11483.966 Million cell updates/sec

Scoring table: OLIGO\_NUC Gapop 60.0 , Gapext 60.0

\*Searched: 1472140 seqs, 8248589755 residues

Word size :

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

GenEmbl:\* gb\_ph:\* gb\_ov:\* gb\_om:\* gb\_pr:\* gb\_pat:\* gb\_htg:\* gb\_sy:\* gb\_sts:\* gb\_vi:\* gb\_ro:\*

em\_pat:\*
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em\_htgo\_hum:\*
em\_htgo\_inv:\*
em\_htgo\_rod:\* em\_htg\_other:\* em\_htg\_inv:\* em\_htg\_hum:\* em\_un:\* em\_sy:\*

> SOURCE ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS RESULT 12
> AF021108/c
> LOCUS
> DEFINITION
> ACCESSION BASE COUNT ORIGIN FEATURES KEYWORDS VERSION JOURNAL MEDLINE JOURNAL TITLE TITLE source Eur. J. F 98454304 2 (bases 1 to 236)
> Philibert,R.A., Horelli-Kuitunen,N., Robb,A.S., Lee,W.Y.-H.,
> Long,R.T., Damschroder-Willlams,P., Martin,B.M., Brennan,M.B.,
> Palottie,A. and Ginns,E.I. Long, R.T., Damschroder-Williams, P., Martin, B.M., Brennan, M.B., Palotie, A. and Ginns, E.I.
> The characterization and sequence analysis of thirty CTG-repeat Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 236)
> Philibert,R.A., Horelli-Kuitunen,N., Robb,A.S., Lee,Y.H., Homo sapiens trinucleotide repeat CTG-13, sequence tagged site.  ${\tt AF021108}$ Submitted (28-AUG-1997) Clinical Neuroscience Branch, National Institutes of Mental Health, 49 Convent Drive Rm BlEB16, Bethesda, STS Direct Submission Homo sapiens AF021108.1 GI:3015581 AF021108 MD 20892, USA containing genomic cosmid clones 26 a Hum. Genet. 6 (1), 89-94 (1998) /note="primers to amplify repeat: forward:
> AAGAGAACCCTCGGCTGGCTCCGG; reverse:
> TTTCTCAGCCCAGCTGCAGCTCC"
> 65 c 72 g 73 t /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="22" Location/Qualifiers 236 bp DNA 03-APR-1998

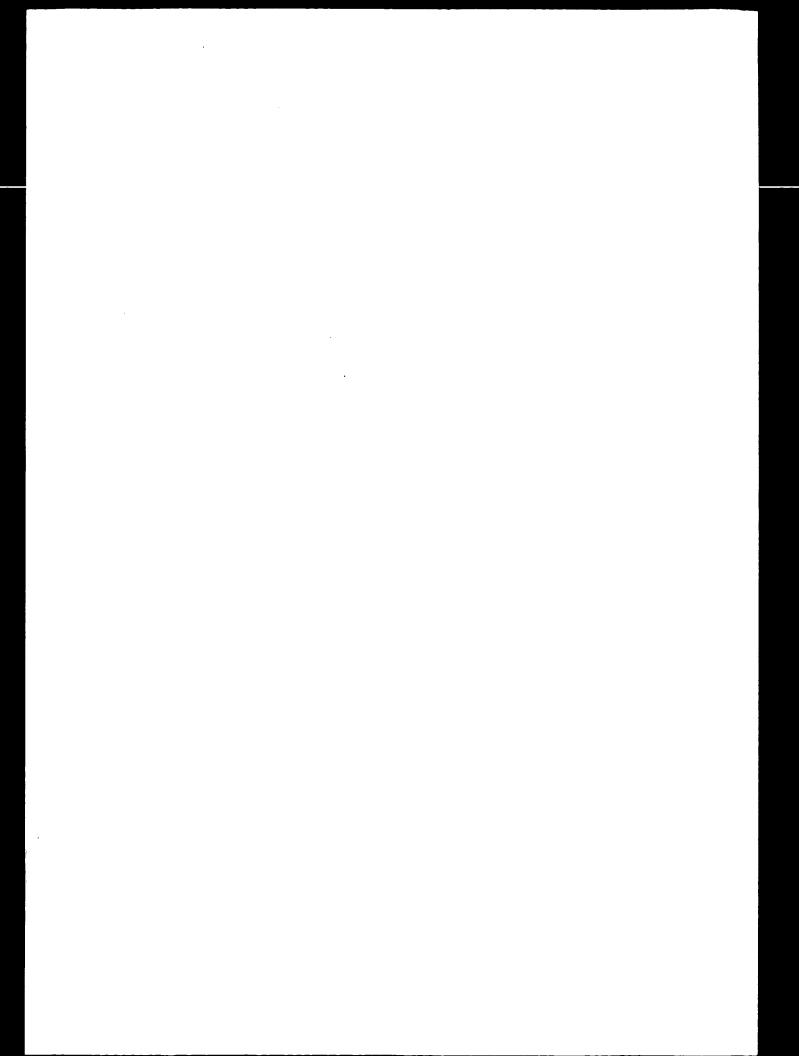
Query Match 4.9%; Score 86; DB 11; Best Local Similarity 100.0%; Pred. No. 4.5e-31; Matches 86; Conservative 0; Mismatches 0; Length 236; Indels 0; Gaps 0

В Qγ 

Qy 584 ttaaattgcatcatcaaaatcagcaa 609

TTAAATTGCATCATCAAAATCAGCAA 1

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Perfect score:
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Maximum DB seq length: 200000000
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  April 30, 2002, 19:51:03; Search time 2499.58 Seconds (without alignments) 11483.966 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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W47924 Human chrom X6602 M.musculus M2364 Rat androge 109480 Sequence 2 M88300 Mouse brain 109511 Sequence 3 M20133 Rat androge AC071063 Mus Muscu M29286 D. virilis e AC079531 Mus muscu L47974 Bos taurus	Human H.sapi Human Human 8 Sequ Purifi 77 Sequ Purifi 9 Huma 12 Homc	500 H 5313 52 Pa 52 Pa 92 6 4 H.s 572 H 572 H 6 H.s 270 F	ALJS9452 HOMO Sapi ALJS8856 Homo Sapi AC007050 Homo sapi AC004033 Homo sapi AK000003 Homo sapi ALJS9452 Homo sapi AX071270 Sequence AF021108 Homo sapi	ription

## ALIGNMENTS

AUTHORS	REFERENCE	PUBMED	JOURNAL			TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF056191	RESULT 1
Abraham, S. and Solomon, W.B.	2 (bases 1 to 3334)	11024300	Gene 255 (2), 389-400 (2000)	tissues	(TIG-1), preferentially expressed in placental and bone-marrow	A novel glutamine-rich putative transcriptional adaptor protein	Abraham, S. and Solomon, W.B.	1 (bases 1 to 3334)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;</pre>	Homo sapiens	human.		AF056191.1 GI:3037134	AF056191	Homo sapiens TPA inducible protein mRNA, complete cds.	AF056191 3334 bp mRNA PRI 11-OCT-2000		

TITLE

Direct Submission

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TPA inducible gene; TIG-1"
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Novelli, G. and Meisterernst, M.
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/protein_id="AAK58423.1"
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/db_xref="G1:14276857"
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                                                                                                   Submitted (02-DEC 1996) Psychiatry, Johns Hopkins Univ. Sch. Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205,
                                                                                                                                                Direct Submission
                                                                                                                                                        Margolis,R.L., Abraham,M.R., Gatchell,S.B., Li,S.H., Kidwai,A.S. Breschel,T.S., Stine,O.C., Callahan,C., McInnis,M.G. and Ross,C.
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Margolis,R.L., Abraham,M.R., Gatchell,S.B., Li,S.H., Kidwai,A.S.
Breschel,T.S., Stine,O.C., Callahan,C., McInnis,M.G. and Ross,C.
cDNAs with lorg CAG trinucleotide repeats from human brain
Hum. Genet. 1(0 (1), 114-122 (1997)
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                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chrcmosome="20"
    /tissue_type="cerebral cortex"
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1163 cgtccccgcagcccggccagcccagctcacagcccaactccaacgtcagctctggccctg 1222
                                                    1043 aggctgcccagatggtggctcccggagtccaggtccagagccagagcctccccatgctgt 1102
                                   569 AGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGT 628
                                                                                                                                                                                   449 TCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGG 508
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/gene="CTG7a"
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388 c 251
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RKKDLSKMKSLLDGI"
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                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.csries: IRAL Plate: 22 Row: n Column: 21
This clone was selected for full length sequencing because it in the column of the column is a column of the column in the column of the column is a column of the column of t
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Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 2106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                the following selection criteria: matched mRNA gi: 7209306
                             /db_xref="taxon:9606"
/clone="IMAGE:3350171"
/tissue_type="Bye, retinoblastoma"
/clone_lib="NIH_MGC_16"
                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone IMAGE: 3350171, mRNA, partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                    at: http://image.llnl.gov
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1731 ccagccatga 1740
                                                                                                                                                       gccgtcctggccaacatccgctcacctgtcttcaaccattccctgtaccgcacattcgtt 1730
                                                                                                                                                                                                                                                                          cccccaccgcccccggtgccaccgaccaaacagcagtacctatgccagccgctcctggat 1670
                                                                                                                                                                                                                                                                                                                                                                                                        accttgcaaaagtgtgagatcgccctggagaaactcaagaatgacat-gcggtgcccact 1610
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CCAGCCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAAAAAAAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccctcacctggacctttaaacacaccctgtgaaccccagctctgtcatgagcccagctggc 1371
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                                                                                                                       GCCGTCCTGGCCAACATCCGCTCACCTGTCTTCAACCATTCCCTGTACCGCACATTCGTT
                                                                                                                                                                                                                                              CCCCCACCGCCCCCGGTGCCACCGACCAAACAGCAGTACCTATGCCAGCCGCTCCTGGAT
                                                                                                                                                                                                                                                                                                                                                                        ACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGGCGGTGCCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGCCCAGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCACCGCAGCCCTCCCAGAGCCCCAGTGACGGCGCGGGACCCCACAGAACTTCAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCCAACTCCAACGTCAGCTCTGCCCCTGCCCCATCTCCCCAGTAGCTTCCTGCCCAGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCCGCAGTCGATGCCCCCCCCCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCCAGCTCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAAG
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/protein_id="AAH07529.1"
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KMKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVFTPPPPPVPFTKQQYLCQPLL
DAVLANITRSPVENHSLIRTFVPAMTAIHGPPITAPVVCTRKRRLEDDERQSIPSVLQG
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RQWQYDANPFLQSVHRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA"
1 719 c 553 g 378 t
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<1. .1157</pre>
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Pred. No. 3e-259;
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64231 bp

13-JUN-2001

COMMENT

REFERENCE

AUTHORS TITLE JOURNAL KEYWORDS SOURCE

ORGANISM

ACCESSION

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Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 52454 bases at least Q30 Consensus quality: 57067 bases at least Q30 Consensus quality: 59753 bases at least Q20 Insert size: 62331; sum-of-contigs Insert size: 190157; 8.2% error; agarose-fp Quality coverage: 2.09x in Q20 bases; sum-of-contigs Coverage: 1.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clcnerequest@sanger.ac.uk on Aug 27, 2000 this sequence version replaced gi:9864141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 1 clone RP11-422P18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Sanger Centre
Center code: SC
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AL359452.4 GI:9930964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently * consists of 20 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: bA422P18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: humcuery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_CANCELLED
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
       27604 2;703; gap off 200 bp; 27704 30911; contig of 3208 bp in length 30912 31011; gap of 100 bp in length 31012 35721; contig of 4710 bp in length 35722 3;821; gap of 35822 38454; contig of 2633 bp in length 38425 3;524; gap of 100 bp 38525 41225; contig of 2671 bp in length 41226 4:325; gap of 100 bp 41326 4:325; g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10077 125
12532 12631:
48067 48166: gap of
                                                                                                                                                                                                                                                                                                                                           24802 24901
24902 27
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21885 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 2992: contig of 2992 bp in length
2993 3(92: gap of 100 bp
3093 5136: contig of 2044 bp in length
5137 5:36: gap of 100 bp
7850: contig of 2614 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5237 7850: contig of 2614 bp in length
7851 7550: gap of 100 bp
7951 9976: contig of 2026 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9977 10076:
                                                                                                                                                                                                                                                                                                                             100 pp
11531: contig of 2455 bp in length
11631: gap of 100 bp
14688: contig of 2057 bp in length
14788: gap of 100 bp
118056: contig of 3268 bp in length
1156: gap of 100 bp
12784: contig of 3628 bp in length
21784: contig of 3628 bp in length
21884: gap of 100 bp
21884: gap of 100 bp
21895: contig of 2917 bp in length
24901: gap of 100 bp
2703: can of 100 bp
                                                                                                                                                                                                                                                                                                                         27603:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                              Query Match
42252 AGATACAGCAGCAGCAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAACAGC 42311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                671 aacagcagcagcagcagcagcagcagcagcagcagcaggctttggaggcccagccaccaa 730
                                                                                                                                                            611 agatacagcagcagcagcagctgcagctgcagcgaatagcacagctgcagctccaacaacagc 670
                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          ture 61882. .64231
    /note="assembly_fragment:00888"
14974 a 15771 c 16128 g 15446 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48167 52656: contig of 4490 bp in length
52657 52756: gap of 100 bp
52757 54927: contig of 2171 bp in length
54928 55027: gap of 100 bp
55028 57420: contig of 2393 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57421 57520:
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:00748"
55028. .57420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:00374"
27704. .30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:00827"
57521. .61781
.note="assembly_fragment:00886"
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12632. .14688
/note="assembly_fragment:00147"
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fragment_chain:1"
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:00199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"assembly_fragment:00098".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment:00698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment:00677"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:00573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:00517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_fragment:00450"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp
contig of 4261 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 2350 bp in length.
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AL358856/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 aggcgcaagctctccctggacaaatgttgtataccccaaccaccactgaaatttgt 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTGT 42606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCAC 42551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Consensus quality: 152367 bases at least Q40 Consensus quality: 153799 bases at least Q30 Consensus quality: 154743 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:9214244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 1 clone RP11-4G23, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 155580; sum-of-contigs
Insert size: 165281; 6.3% error; agarose-fp
Quality coverage: 5.20x in Q20 bases; sum-of-contigs Quality
coverage: 4.91x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL358856.3 GI:9863846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL358856
                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bA4G23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                                                                                                                  runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                  3464 3563; gap of 100 bp
3564 13200; contig of 9637 bp in length
13201 13300; gap of 100 bp
13201 13300; gap of 100 bp
13301 59189; contig of 45889 bp in length
                                                                            59190 59289:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157080 bp
59289: gap of 100 bp
85824: contig of 26535 bp in length
85924: gap of 100 bp
88142: contig of 2218 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
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В Qy В

75506 AGATACAGCAGCAGCAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGC 75447

611 agatacagcagcagcaacagctgcagctgcagcgaatagcacagctgcagctccaacaacagc 670

75446 AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGCTTTGCAGGCCCAGCCAA 75387

731 ttcagcagccaccgatgcagcagccacagcctccgccctcccaggctctgccccagcagc 790

671 aacagcagcagcagcagcagcagcagcagcagcagcagcctttggaggcccagccaccaa 730

Query Match Best Local Matches

Similarity

17.5%; 99.7%;

Score 304; DB 2; Pred. No. 9.6e-139; Mismatches

DB 2;

Length 157080; Indels

0.

Gaps

0

354;

Conservative

0;

8

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FEATURES
  BASE COUNT
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88243 95033: contig of 6791 bp in length
95034 95133: gap of 100 bp
95134 100091: contig of 4958 bp in length
100092 100191: gap of 100 bp
117326: contig of 17135 bp in length
117327 117426: gap of 100 bp
117427 11946: contig of 2520 bp in length
119947 120046: gap of 100 bp
119947 120046: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130610 139309; contig of 8700 bp in length
139310 139409; gap of 100 bp
139410 157080; contig of 17671 bp in length
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/note="assembly_fragment:01664
fragment_chain:1"
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/note="assembly_fragment:01204
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                         85925.
                                                                                                                                                                                                 /note="assembly_fragment:00869
fragment_chain:2"
117427. .119946
                                                                                                                                                                                                                                                            /note="assembly_fragment:01408
fragment_chain:2"
100192. .117326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:left"
/note="assembly_fragment:01779"
39841 c 39467 g 39369 t 1
                                           139410. .157080
                                                                                130610. .139309
                                                                                                                                           120047. .130509
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                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:01296
fragment_chain:2"
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                                                                                                                                                                                                                                                                                                                                                                                                  fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00057
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                              /note="assembly_fragment:01620
fragment_chain:3"
                                                                                                                                                        /note="assembly_fragment:00628
fragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:00505
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-4G23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                       /note="assembly_fragment:01199"
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130509: contig of 10463 bp in length
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      1101 others
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75386 TTCAGCAGCGACGGATGCAGCACACAGCCTCCGGCCTCCCAGGCTCTGCCCCAGCAGC 75327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75206 AGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTGT 75152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75326 TGCAGCAGATGCATCACACACAGCACCAGCCGCCACCACCAGCCCCAGCAGCCTCCAG 75267
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                                                                                                                       Chen, F., Hu, X., Budari, M., Emanuel, B. and Noc.,.....
Direct Submission
Submitted (26-AUG-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                     Chen,F., Hu,X., Budart,M., Emdnuet,D., and Direct Submission
Submitted (22-JUL-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, F., Hu, X., Budarr, M., Emanuer, D., Chenistry, And Biochemistry, Submitted (07-JUL-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
  Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A. Direct Submission
Submitted (01-SEP-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
                                                                                                                                                                                                                                                                         Submitted (29-JUL-1999) Department Of Chemistry And Biochemistry, The Universit, Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                       Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (19-3UL-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen.F., Hu.X., Emanuel.B., Budarf,M. and Roe.B.A.
Direct Submission
Submitted (09-MAR-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 163908)
Chen,F., Hu,X., Budarf,M., Emanuel,B. and Roe,B.A.
Homo, sapiens Chromosome 22q11 BAC Clone bac32 In BCRL2-GGT Region
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                                                                                                           (bases 1 to 163908)
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                                                          Region, complete sequence. AC004033
                                      AC004033.3 GI:4581183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22q11"
/clone="bac32"
/a 41642 c 42088 g 40851 t
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99.7%;
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14859 AGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACCTGAAATTTTGT 14913
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                                                                                                                                                                                                                                                                                                                                                                                   14799 TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCAC 14858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14679 TTCAGCAGCCGATGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGC 14738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14619 AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCAGGCTTTGCAGGCCCAGCCACCAA 14678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14739 TGCAGCAGATGCATCACACACAGCACCAGCCGCCACCACAGCCCCAGCAGCCTCCAG 14798
                                                                                                                                                                                                                                                                                                        911 aggcgcaagctctccctggacaaatgttgtatacccaaccaccactgaaatttgt 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 agatacagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaacagc 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 ttcagcagccaccgatgcagcagccacagcctccgccctcccaggctctgccccagcagc 790
                                                                                                                                                                                                                                                                                                                                                                                                                                    ttgctcagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtcac 910
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ON NOV 20, 1999 this sequence version replaced gi:6067157.

Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

AC004033(p_ml1) 89227 145356 (0) overlaps AC007050(bac32) 1 59304 (104604) AC007050(bac32) 141234 163908 (0) overlaps
AC004033 145356 bp DNA PRI 31-MAY-200
Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT
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11 (bases 1 to 163908)
Chen,F., Hu,X., Budarf,M., Emanuel,B. and Roe,B.A.
Direct Submission
Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 (bases 1 to 163908)
Chen.F., Hu.X., Budarf,M., Emanuel,B. and Roe,B.A.
Direct Submission
Submitted (19-OCT-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-NOV-1999) Department Of Chemistry And Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, F., \operatorname{Hu}_{\mathsf{X}}, \operatorname{Budarf}_{\mathsf{M}}, \operatorname{Emanuel}_{\mathsf{B}}, and \operatorname{Roe}_{\mathsf{B}}. A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 304; DB 9;
Pred. No. 9.5e-139;
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REFERENCE
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OR Apr 12, 1999 this sequence version replaced g1:4580479.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.
AC005500(p52f6) 112352 192592 (0) overlaps AC004033(p_m11) 1 78509 (66847) AC004033(p_m11) 89227 145356 (0) overlaps AC007050(bac32) 1
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Zhang,G., Lao,V., Zhan,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-DEC-1998) Department Of Chemistry The University Of Oklahoma, 620 Parrington Oval.
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                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                9 (bases 1 to 145356)
2hang,G., Lao,V., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A
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Submitted (12-APR-1999) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OK 73019,
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Direct Submission
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                                                                                       /clone="p_m11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-63'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3913, Fax:81-438-52-3914)
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Research, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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Ohara,O., Kikuno,R., Nagase,T. and Okumura,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-FEB-2000) to the DDBJ/EMBL/GenBank databases. Osamu
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                                                                                                                                                        /note="For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone is
/product="FLJ00003 protein"
/protein_id="BAA92228.1"
/db_xref="GI:7209307"
                                                                                                           Start codon is not identified
                                                                                  /codon_start=1
                                                                                                                                       accessible through http://www.kazusa.or.jp
                                                                                                                                                                                                                                           /gene="FLJ00003"
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                                                                                                                                                                                                                                                                                                                                                 /note="vector: pBluescriptII SK plus"
                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="spleen"
                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
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/db_xref="taxon:9606"
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Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dys-terminator Big Dye; 100% of reads
Consensus quality: 52454 bases at least Q40
Consensus quality: 57067 bases at least Q20
Consensus quality: 59753 bases at least Q20
Insert size: 12331; sum-of-contigs
Insert size: 120157; 8.2% error; agarose-fp
Quality coverage: 2.09x in Q20 bases; sum-of-contigs Quality
Coverage: 1.09x in Q20 bases; agarose-fp
* NOTE: This ..s a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. (aps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9864141.
                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: 3C
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Mammalia; Eut.eria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64231)
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Homo sapiens chromosome 1 clone RP
PROGRESS ***, 20 unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk
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100.0%; Pred. No. 7.7e-89;
7ative 0; Mismatches 0;
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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48167 52656; contig of 4490 bp
52657 52756; gap of 100 bp
52657 54927; contig of 2171 bp
54928 55027; gap of 100 bp
55028 57420; contig of 2393 bp
55028 77420; contig of 2393 bp
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2993 3092: gap of 100 bp
3093 5136: contig of 2044 bp in length
5137 5236: gap of 100 bp
7850: contig of 2614 bp in length
/note="assembly_fragment:00374"
27704. .30911
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18157. .21784
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12632. .14688
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7951. .9976
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fragment_chain:1"
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/db_xref="taxon:9606"
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61781: contig of 4261 l
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41225: contig of 2671 bp in length
325: gap of 100 bp
48066: contig of 6741 bp in length
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38454: contig of 2633 |
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contig of 2614 bp in length
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                                                      232;
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                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 386)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
                                                                                                                                                                                                                                               Human genes and gene expression products Patent: WO 0102568-A 1742 11-JAN-2001; CHIRON CORPORATION (US); HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX071270.1
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48167. .52656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00573"
41326 .48066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:00827"
57521. .61781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:00450" 35822. .38454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00401"
31012. .35721
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
88 c 138 g 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00888"
15771 c 16128 g 15446 t 1
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55028. .57420
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                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:00886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:00517"
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100.0%; Pred. No. 1.9e-56;
tive 0; Mismatches 0;
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                                                      0;
                                                                   Score 132; DB 6; Length 386; Pred. No. 9.3e-54;
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                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 CACAGCACCACCAGCCGCCACCAGCCCCAGCAGCCCCCAGTTGCTCAGAACC 15
                                                                                                                                          26 TTANATTGCATCATCAAAATCAGCAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAGCAGCAGCAGCAGGCTTTGCAGGCCCAGCCACTATTCAGCAGCCTCCGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATVALIUS 236 bp DNA STS (Homo sapiens trinucleotide repeat CTG-13, sequence AF021108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 236)
Philibert, R.A., Horelli-Kuitunen, N., Robb, A.S., Lee, Y.H., Long, R.T., Damschroder-Williams, P., Martin, B.M., Brennan, J. Palotie, A. and Ginns, E.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-AUG-1997) Clinical Neuroscience Branch, National Institutes of Mental Health, 49 Convent Drive Rm BlEE16, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 236)
Philibert, R.A., Horelli-Kuitunen, N., Robb, A.S., Lee, W.Y.-H., Philibert, Damschroder-Williams, P., Martin, B.M., Brennan, M.B., Palotie, A. and Ginns, E.I.
AC005500
                sequence
                               Homo sapiens 22q11 PAC Clone Clone p52f6
                                                   AC005500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Eur. J. Hum. Genet. 6 (1), 89-94 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The characterization and sequence analysis of thirty CTG-repeat
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Mammalia; Eutheria; Primates;
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AAGAGACCCTCGGCTGGCTCCG; reverse:
TTTCTCAGCCCAGCTGCAGCTCC'
1 65 c 72 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                 192592 bp
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                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                  Score 86; DB 11; 1; Pred. No. 4.5e-31;
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                                 DGCR Region, complete
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                                                   31-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen,F., D,L., Do,T., Dumanski, .... and No., .....
Direct Submission
Submitted (3)-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                   Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
Direct Submission
Submitted (0:-NOV-1998) Department Of Chemistry And Biochemistry,
Submitted (0:-NOV-1998) Department Of Chemistry And Biochemistry,
The Total Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen, F., D, L., Do, T., Dumanski, J.P. and Roe, B.A.

Direct Submission
Submitted (23-0CT-1998) Department Of Chemistry And Biochemistry, Submitted (23-0CT-1998) Department Of Chemistry And Biochemistry, Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry Of Oklahoma, 620 Parrington Oval, Room 208, Norman, Chemistry Oval, Room 208, Norman, C
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Direct Submission
Submitted (14-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 (bases 1 to 192592)
Chen, F., D, L., Do, T., Dumanski, J.P. and Roe, B.A.
Direct Submission
Submitted (01-OCT-1998) Department Of Chemistry And Biochemistry,
Submitted (01-OCT-1998) Department Of Chemistry And Biochemistry,
Ok 73010
Chen, F., D, L., Do
Direct Submission
                                                      OK 73019, USA
12 (bases 1 to 192592)
                                                                                                                                                           Submitted (21-NOV-1998) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                      Direct Submission
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Direct Submission
Submitted (01-OCT-1998) Department Of Chemistry And Biochemistry,
Submitted (01-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 192592)

Chen.F., D.L., Do.T., Dumanski, J.P. and Roe, B.A.

Direct Submission
Submitted (23-SEP-1998) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-SEP-1998) Department Of Chemistry And Biochemistry, or University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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1 (bases 1 to 192592)
Chen.F., D.L., Do.T., Dumanski,J.P. and Roo. B.
                                                                                                                        The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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                                                                                                                                                                                                                                        Submitted (02-FEB-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany This sequence is part of a larger genomic contig. The start of the sequence is directed towards the centromere. The end (107393. 107642) of this sequence overlaps with the start of the neighboring sequence deposited in GenBank Accession Number and Participated.
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Platzer,M., Zhao,W., Herman,G.E. and Rosenthal,A.
Comparative sequence analysis of the mouse Mtm locus and the corresponding region of human Xq28
Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Direct Submission
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Because these overlapping clones came from different libraries
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/clone="p52f6"
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/clone_lib="CitbCJ7 [129/Sv]" 607. .645
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                          Parachartergis colobopterus.

Parachartergis colobopterus

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Nioptera; Endopterygota; Hymenoptera; Apocrita;

Aculeata; Veipoidea; Vespidae; Polistinae; Parachartergus.

1 (bases 1 :0 164)

Strassmann, J.E., Solis, C.R., Barefield, K. and Queller, D.C.

Trinucleotid; microsatellite loci in a swarm-founding neotropical wasp, Parachirtergus colobopterus and their usefulness in other social wasps

Mol. Ecol. 5 (3), 459-461 (1996)
                                                                                                                                                                                                                                                                                                           2 (bases 1 To 164)
Strassmann, J.E., Hughes, C.R., Barefield, K., Solis, C.R. and Queller, D.C.
                                                                                                                                                                                                                                         Direct Submission
Submitted (13-JUL-1996) Ecology & Evolutionary Biology, Rice University, '5100 Main, Houston, TX 77005, USA Location/Qualifiers
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complement(35049...35112)

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complement(38944. .38977)
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Search completed: April 30, 2002, 21:39:54 Job time: 6531 sec

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Copyright (c) 1993 - 2000 Comp
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## ALIGNMENTS

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PR 19-1 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317. 09-JUL-2000; 2000US-0598042. 19-JUL-2000; 2000US-0620312. 03-AUG-2000; 2000US-0653450. 14-SEP-2000; 2000US-0653036. 19-OCT-2000; 2000US-0727344. Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; Human polynucleotide SEQ ID NO 1658. AAI59455; AAI59455 standard; cDNA; 2556 BP 26-JUL-2001 WO200153312-A1 Homo sapiens. chemokinetic; 22-OCT-2001 26-DEC-2000; 2000WO-US34263 leukaemia; ss. -(first entry) thrombolytic; drug screening; arthritis;

inflammation;

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818 cagcagttccaggctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcag
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RESULT
AAI61241
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Inmune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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09-JUL-2000;
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03-AUG-2000;
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19-OCT-2000;
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the fusion protein is compared to the human protein only. The genes are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adtenal gland, bone, born marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune
                                                                                                                                                                    The invention relates to the isolation of genes AAA58990-A59039 encoding 50 human secreted proteins AAB27560-B27609. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
neurological disease; infection; human; secreted protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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11-JUN-1999;
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99US-0138574.
99US-0168667.
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disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                              haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
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Sequence 1388 BP; 364 A; 378 C; 343 G; 297 T; 6 other;

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Similarity

44.78; 99.78;

Pred. Score 777; Pred. No. 0;

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962 ccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcgcaagctctc
                    865 ccatcacaactcccgccacagtcgccagacccagcctttggtgtcacaggcgcaagctctc
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                                                                                                                                                                                                                                                                                               microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022
                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 9950; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                    Sequence 316
                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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26-MAY-2000;
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                                                                                            374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
    494
                                                        434
                             61
                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagcagctcc 553
                                          agcagcagcaggcggcgctacagcagcagcagcagcagcagcagcagcagcagcagttccagg 493
                          agcagcagcagcgcgctacagcagcagcagcagcagcaacagcagcagttccagg
                                                                               cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-488901/53.
                                                                                                                                      239;
                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                         gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                     BP; 81 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                     104 C; 87
                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                              Score 239; DB 22;
Pred. No. 1.4e-99;
                                                                                                                                                                                                                                                                                                                                                                                                        human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                     Mismatches
                                                                                                                                                                                                       ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1051
                                                                                                                                                                                                       44 T; 0 other;
                                                                                                                                                            Length 316;
                                                                                                                                     Indels
                                                                                                                                   0;
                                                                                                                                  Gaps
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RESULT
AAI45215
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                                                                                                                                        Query Match
Best Local Sin
Matches 239;
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                 Sequence 316 BP;
                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #13901 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI45215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI45215 standard; DNA;
                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray;
 121
                       494
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                                                                                                     374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacag
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           agcagcagcaggcggctacagcagcagcagcagcagcagcaacagcagttccagg
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                                             agcagcagcaggcgctacagcagcagcagcagcagcagcaacagcagttccagg
                                                                                        cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagttccagc 60
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                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                      genome-derived single exon nucleic acid
zing gene expression in human placenta -
                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                           SEQ ID No 13901; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Hanzel
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2000US-0234687.
2000US-0236359.
                                                                                                                                         Conservative
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                  expression
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                                                                                                                                                                                                 81 A; 104 C; 87 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; placenta;
                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                  in human placenta
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                                                                                                                                                   Score 239; DB 22;
Pred. No. 1.4e-99;
                                                                                                                                                                                                                                                                                                                                                                              Rank DR
                                                                                                                                         Mismatches
                                                                                                                                                                                                  44 T; 0 other;
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                                                                                                                                         0;
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                                                                                                                                                              Length 316;
                                                                                                                                         Indels
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26-MAY-2000; 2000US-0068408.

30-JUN-2000; 2000US-0632366.

21-SEP-2000; 2000US-0532366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0234585.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene, expression in a human breast sample, where the probybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those ciseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the better the beautiful to the problem.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 316 BP; 81 A; 104 C; 87 G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence (ata for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the breast, fibrocystic changes, proliferative breast disease and {\tt non\textsc{-}carcinoma\ tumours}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 5716; 322pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disease; proliferative breast disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #5716 used to measure gene expression in human breast sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in a human breast
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                           434 agcagcagcaggcggcgctacagcagcagcagcagcagcagcaacagcagcagttccagg 493
                                                                                                                                                                  374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcaaccagcagcagttccagc 433
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   61
                                                                                                                               1 cccagctgcagctcuagcaggtggcgctgcagcagcagcagcaacagcagcagttccagc 60
                                                                                                                                                                                                                                                                                                          Loca.
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agcagcagcaggcg@cgctacagcagcagcagcagcagcaacagcagcagttccagg 120
                                                                                                                                                                                                                                                                           239;
                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                              Score 239; DB 22; pred. No. 1.4e-99;
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434 agcagcagcaggcgctacagcagcagcagcagcagcaacagcagcagttccagg 493

374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagcagttccagc 433

187 cccagctgcagctccagcaggtggcgctgcagcagcagcagcaacagcagttccagc 246

Matches Query Match

Local Similarity 100 les 239; Conservative

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26-MAY-2000; 2000US-0207456.
30-JUN_2000; 2000US-0632366.
21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234589.
04-OCT-2000; 2000GB-0024263.
                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
Sequence 436 BP; 105 A; 127 C; 117 G; 87 T; 0 other;
                                 at ftp.wipo.int/pub/published_pct.
                                                                                                                                                                                                                           Claim 25; SEQ ID No 708; 487pp; English.
                                                                                                                                                                                                                                                         analyzing gene expression in human
                                                                                                                                                                                                                                                                                                               WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cervical cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #708 for gene expression analysis in human cervical cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #719 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI32033 standard;
                                                                                                                                                                                                                                                                                                              Sequence 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554
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                                                 434
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  247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agcagcagcaggcgctacagcagcagcagcagcagcagcaacagcagcagttccagg
                                                                                                                  cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaattcagcaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagctcc
agcagcagcaggcgctacagcagcagcagcagcagcagcaacagcagcagttccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-488897/53.
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                                                                                           cccagctgcagctccagcaggtggcgctgcagcagcagcagcaacagcagcagttccagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for
zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to single exon nucleic acid probes (SENP).
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         BP; 105 A; 127 C; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; placenta; antenatal diagnosis;
                                                                                                                                                                                  13.7%; sur
100.0%; Pr
.... 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                       Score 239; DB; Pred. No. 1.4.0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                            G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                placenta
                                                                                                                                                                                                             1.4e-99;
                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                          0;
                                                                                                                                                                                                                                    Length 436;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                               probes are
                                                                                                                                                                                          0;
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                               493
                                                                                                                                                                                                                                                                                                                                                                                    useful
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                                                                                           246
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B 68

187

374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcaacagcagctacagc 433

cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagttccagc

Matches

Query Match Best Local Similarity

13.7%; So illarity 100.0%; F Conservative 0;

Score 239; DB 22; Pred. No. 1.4e-99; 0; Mismatches 0;

Length 436; Indels

0;

Gaps

0

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RESULT
AAI00701
ID AAI
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                                                                                  measuring human gene expression in a human breast sample, where the problem that the human hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #692 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI00701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI00701 standard;
Sequence 436 BP; 105 A; 127
                                           Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                        Novel single exon nucleic
                                                                                                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disease;
                                                                         non-carcinoma tumours.
                                                                                                                                                                                                                                                              in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
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                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                     present invention relates to novel single exon nucleic acid probes. present sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agcagcagcagcagcagcagcatctaattaaattgcatcatcatcaaaatcagcaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcagcagagtgccatgcagcagtagttccaagcagtagtgcagcagcagcagcagcacc
                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                      SG,
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                                                                                                                                                                                                                                                                                                         2001-476286/51.
                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS
                                                                                                                                                                                                                                 SEQ ID No 692; 322pp; English.
                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                              breast
                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                          acid probe used
   C; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                      Rank DR;
   ç;
   87 T; 0
                                                                                                                                                                                                                                                                             to measuring gene expression
                                           ot form
format
    other;
                                           part of the directly from
                                                                                                                                                                           the probe
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                                              WIPO
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Qy Дb QΥ Дb δÃ

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494 ctcagcagagtgccntgcagcagcagttccaagcagtagttgcagcagcagcagcagctcc 553

307 ctcagcagagtgccntgcagcagcagttccaagcagtagtgcagcagcagcagcagctcc 366

Novel human polynucleotide, SEQ ID NO: 1742.

breast cancer; lung cancer; cancer detection; ss

cytostatic; gene therapy; colon cancer;

prostate cancer;

09-APR-2001

(first entry)

AAF65986;

AAF65986 standard; cDNA; 386 BP

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Best Local Similarity 99.1%;
Matches 232; Conservative
                                             The present sequence is one of a large number of 5′ ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5′ ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3′ untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5′ ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5′ UTR is rarely included. 5′ ESTs are derived from mRNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5′ ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 13446; 71pp + CD-ROM; English.
                                      expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC09371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC09371 standard; cDNA; 232 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AGCAGCAGCAGCAGCAGCCAGCCAGCCACCAATTCAGCAGCCTCCGATGC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             689 agcagcagcagcagcagcagctttggaggcccagccacttcagcagccaccgatgc 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 agcagctgcagcgaatagcacagctgcagctccaacaacagcaacagcagcagcagcagc 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A, Giordano J;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 132; DB 22;
Pred. No. 1.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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RESULT 10
AAAF65986/c
ID AAAF6599
XX AAF659
XX OAAF659
XX O9-APR
XX UP-APR
X

02-JUL-1999; 02-JUL-1999;

99US:0142310. 99US:0142311.

30-JUN-2000; 2000WO::US18374.

11-JAN-2001 WO200102568-A2. Homo sapiens

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

WPI; 2001-091805/10.

Williams LT, Escobedo J, Innis MA, Garcia PD, Klinge Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Crkenjakov R, Drmanac S, Dickson M, Labat I, Leshkov Kita D, Garcia V, Jones LW, Strache-Crain B;

Leshkowitiz Klinger J,

Drmanac R; Kassam A;

Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -

Claim 9; Page 793; 1.046pp; English.

The present sequence is one of 3331 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligon.cleotides can be generated. The polynucleotides and their gene products are used as generated. The polynucleotides and blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,

Sequence 386 BP; 50 A; 88 C; 138 G; 110 T; 0 other;

Sequence 232 BP; 52 A; 53 C; 87 G; 37 T; 3 other

dysplasia and hyperplasia.

Query Match

Length 232;

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Вb
                          QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                This represents a sequence encoding glutamine rich repeat region which can be found in spinocerebellar ataxia type 2 (SCA2) patients. The specification provides a gene sequence causative of the neurodegenerative disease SCA2, having a tri-nucleotide (CAG) repeat region which in the expression product produces a polyglutamine sequence from Gln-166 to Gln-188. In the normal gene there are 15-25 CAG repeats but in SCA2 patients this number is increased to 35-100. Peptides encoded by nucleic acid fragments (DNA or RNA) containing sequences from the SCA2 associated gene, antibodies recognising the peptides and antisense nucleic acids hybridising with the nucleic acid fragments can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spinocerebellar ataxia type 2; CAG repeat; neurodegenerative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glutamine rich region encoding
                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid fragments associated with spinocerebellar ataxia type - contain increased number of CAG repeat region compared to normal
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-272215/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1996;
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                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                            Example 1; Page 22; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SRLS-) SRL INC
                                                                                                                                                      Investigation and diagnosis of SCA2. They can also be used for the creatment of SCA2 by antisense therapy or gene therapy.
             220
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                                                       l Similarity
45; Conser
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                                                                                                                             203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.2%; Score 73; DB 21; 1 larity 100.0%; Pred. No. 1.2e-23; Conservative 0; Mismatches 0;
                                                       2.6%;
llarity 100.0%;
Conservative (
                                                                                                                             BP; 68 A;
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                                                                                                                             70
                                                                                                                             c;
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                                                                   Score 45;
Pred. No.
                                                                                                                             62 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence found in SCA2 patients.
                                                                    DB 19; I
. 7.5e-11;
                                                                                  Length 203;
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RESULT 13
AAV17226
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                                                                                                                                                                                                                                                                                                              Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV17226 standard; DNA; 203
                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type the method of the invention for diagnosing two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG parts of the SCA2 gene sequence, and determining the number of CAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCA2 gene;
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                                                                                        TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF; TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                         Transgene for epitope tagged TBP protein.
                                                                                                                                                                        AAV08558;
                                                                                                                                                                                                                                                                                                                                                           Sequence 203 BP; 68 A; 70 C; 62 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                  repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II.
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                                                      Homo sapiens
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                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spinocerebellar ataxis type II; CAG repeat; PCR
                                                                                                                                                                                                                                                                                                  2.6%;
llarity 100.0%;
Conservative (
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Pred. No.
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                                                                                                                                                                                                                                                                                                                        Length 203;
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02-DEC-1998

EP881288-A1. Synthetic.

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 Berglund E,
                                (FARH ) HOECHST AG.
                                                                 26-MAY-1997;
                                                                                                 26-MAY-1998;
                                                                                                                                 02-DEC-1998.
                                                                                                                                                                 EP881288-A1
                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                            TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF; TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                                                                                                                                                                                                           Transgene for epitope tagged TBP protein.
                                                                                                                                                                                                                                                                                                                                             12-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1310 BP; 349 A; 357 C; 306 G; 298 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 24; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic animal expressing epitope-tagged TATA box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-001394/01.
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 Kirschbaum B,
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                                                                 97EP-3108433.
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Meisterernst M,
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 Polites G;
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DR WPI; 1999-001394/01.

XX Transgenic animal expressing epitope-tagged TATA-box binding protein PT for isolating higher-order transcription complexes and specific PT factors that associate with the protein, useful as potential PT factors that associate with the protein, useful as potential PT therapeutic agents

XX Claim 2; Page 27-29; 38pp; English.

XX This sequence encodes an epitope-tagged TATA-box binding protein (TBP) CC that is expressed by the transgenic non-human animals of the invention. CC The animals are used to produce TBP TBP is used to isolate and CC characterise higher-order transcription complexes (from different tissue animals are used to produce TBP TBP is provided to isolate and CC characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also cc used to identify new and/or specific TBP associated factors (TAPS, CC e.g. transcription factors, activators or inhibitors) and TAF-interaction cregulating gene expression, e.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug coreening. The antibodies are used for affinity purification of TBP and CC variety of different tissues and cells (contrast known methods that are CC limited to isolation from a particular cell type).

XX sequence 3263 BP; 860 A; 794 C; 756 G; 853 T; 0 other;
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Gaps

Search completed: April 30, 2002, 20:44:05 Job time: 3286 sec

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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

12	c 11	10	9	8	7	c 6	ъ	4	с 3	2	1	No.	Result
347	357	385	395	399	418	431	450	475	509	551	566	Score	
19.9	20.5	22.1	22.7	22.9	24.0	24.8	25.9	27.3	29.3	31.7	32.5	Match Length DB	Ouerv
757	486	723	886	756	914	482	776	526	620	2752	730	ength	
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AL046886	AW747905	BE279307	BG281923	BG746380	BG468341	AA664125	BG750043	BE019568	BE384305	BC005027	BG766214	ID	
Ų,	_	BE279307 601157640		BG746380 602703648		AA664125 ac06c04.s	BG750043 602708813	BE019568 ba83f05.y		BC005027 Homo sapi	BG766214 602737942	Description	

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121	130	135	136	138	143	158	164	164	169	170	172	181	185	211	216	236	241	242	252	254	255	260	267	267	283	287	292	301	308	319	327	340
	7.5				•	•		•	•										14.5						•						18.8	
301	200	385	568	255	668	443	1043	810	258	348	733	235	939	335	942	434	386	313	391	393	1157	386	428	424	1019	557	656	498	524	878	956	501
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AA069235	BF084780	R17502	в1089323	BF870481	BG766083	BI024741	BF974180	BG686794	BF755836	T07163	BE391135	BF994170	BG336790	в1011820	BG338685	BF346622	BG982761	N49344	AW500833	AW499614	BG177319	BG982754	BE889171	AW501171	BG335275	BG421322	BE390284	AW603679	BE410770	BG386117	12269	351
AA069235 zmlle01.r	BF084780 IL3-CT053	R17502 yg02d12.r1	BI089323 602853282	BF870481 IL3-ET011	BG766083 602738467	BI024741 PM0-MT020	602243	602650	BF755836 CM3-CT057	T07163 EST05052 Fe	BE391135 601286095	BF994170 CM2-GN016	BG336790 602405533	BI011820 PM1-EN006	BG338685 602436442	BF346622 602021224	BG982761 PM0-CN015	/23e10.	AW500833 UI-HF-BP0			שי		_	60240378		BE390284 601285167	CM0-CN00	60130168	_	235182	QV3-HT04

## ALIGNMENTS

RESULT

	source	FEATURES								COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BG766214
/organism="Homo sapiens" /db_xref="taxon:9666" /clone="IMAGE:4862938" /clone_lib="NIH_MGC_49" /tissue_type="melanotic melanoma, high MDR (cell line)" /lab_host="DH10B (phage-resistant)"	1 730	High quality sequence stop: 716.	Plate: LLCM1724 row: d column: 11	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Preparation: Ling Hong/Rubin Laboratory	Tissue Procurement: ATCC/DCTD/DTP	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		human.	EST.	BG766214.1 GI:14076867	BG766214	mRNA sequence.	49 Homo sapiens cDNA clone IMA	BG766214 730 bp mrna EST 15-MAY-2001	

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ACCESSION
KEYWORDS
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                                                                                                   Homo sapiens, clone IMAGE:2822900, mRNA BC005027
                                              BC005027.1 GI:14709725
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1310 tececteactigacetttaaacacactgtaacecagetetgteatgageccagett 1369 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7209306
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Lettlcia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 2752)
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Tissue Procurement: DCTD/DTP
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//db_xref="taxon:9606"
/clone="IMAGE:2822900"
/tissue_type="Lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
/lab_host="DH10B-R"
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905 c 791 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM275 row: g column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                   79
                     /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Lipa (DT1); DT2]
/cloned into EcoRI/XhoI sites using the following 5;
/cloned into EcoRI/XhoI sites using 
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                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3613868"
/clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml

Seq primer: -40RP from Glbco
                                                                                                                                                                                                                                                                                                                                                         BE019568 526 bp mRNA EST 06-JUN-200 ba83f05.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2907009 similar to TR:015413 O15413 CTG7A; mRNA sequence.
                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                             Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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High quality sequence stop: 463
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Pred. No. 4.5e-223;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           BG750043 776 bp mRNA EST 15-MAY-2001 602708813F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845411 5',
                                                            numan.
Homo sapiens
                                                                                                                                   EST
                                                                                                                                                         BG750043.1 GI:14060696
                                                                                                                                                                                                                     mRNA sequence.
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/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; vector: poTB7; Site_1: xhoI;
/note="Organ: placenta; vector: poTB7; Site_1: xhoI;
/note="Organ: placenta; vector: poTB7; Site_1: xhoI;
/note="Organ: placenta; vector: poTB7; Site_sing the
/note="Organ: placenta; vector: placenta; vector: placenta; vector: placenta;
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Pred. No. 1.9e-207;
0; Mismatches 1;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: ATCC
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/Clone_lib="NIH_MGC_43"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented"; Site_1: XhoI; Site_2:
/note="OTGan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="OTGan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="OTGan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
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Location/Qualifiers
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314 286 1810
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/clone="IMAGE:855654"
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Pred. No. 3.1e-187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
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/note="Organ: color; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                           /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_bost="DH10B (phage-resistant)"
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                                                                                                                                                                                   /clone="IMAGE:4644299"
                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                    Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 756)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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BG746380.1 (I:14057033
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                       BG281923 886 bp mRNA EST 21-FEB-2001 602403104F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545433 5',
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               Homo sapiens
                                                                                                                                             BG28192
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/lab_host="DH10B (phage=resistant)"
/note="organ: colon; Vector: pOTB3; Site_1: xhoI; Site_2:
Conet : cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected > 500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
a 264 c 186 g 126 t 1 others
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/clone_lib="NIH_MGC_15"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
mRNA sequence.
BE279307
                                                                                                                                          BE279307 723 bp mRNA EST 13-JUL-2000 601157640F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504608 5',
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Tissue Procurement: ATCC/DCTD/DTP
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: Site of following 5;
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/clone_lib="NIH_MGC_20"
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421 cagcagttccagcagcagcagcggcgctacagcagcagcagcagcagcagcaacag 480
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                                                                      gcaactccacagacccagctgcagctccagcaggtggcgctgcagcagcagcagcaacag
                                                                                                                                                                                                                                                agcctgactggcggacctgctgcgggagccgctgggaattggcatgcctcctcgggggcccg
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                                                                                                                                                              gggcagccgcctcctgggacctcggggatggcccttcacagcatggctgtcgtgtctacg
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                                              GCAACTCCACAGACCCAGCTGCAGCTCCAGCAGCTGGCGCGCTGCAGCAGCAGCAACAG
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM179 row: o column: 09 High quality sequence.stop: 661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates;
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/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; vector: pOTB7; Site_1: xhoI;
/note="Organ: placenta; vector: pOTB7; Site_1: xhoI;
/note="Corgan: placenta; vector: poigo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
77 a 208 C 224 g 114 t
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Pred. No. 4.2e-166;
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838 cagcagcctccagttgctcagaaccaaccatcacaactcccgccacagtcgcagacccag 897
                                                                                                                                                   486 GCCCAGCCAATTCAGCAGCCACCGATGCAGCAGCCACGAGCCTCCGCCCTCCCAGGCT 427
                                                   778 ctgccccagcagctccagcagatgcatcacacacagcaccaccagccgccaccacagccc 837
                                                                                                                                                                                718 gcccagccaccaatt.cagcagccaccgatgcagccacagcctccgccctcccaggct 777
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2-QV1-BN0002-
201299-042-c(16t3=1999-12-20&t4=1)
Seq primer: proc 18 forward.
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1 (Dases 1 to 486)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., (da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares;,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW747905 486 bp mrNA EST 28-APR-2000 QV1-BN0002-201299-042-c01 BN0002 Homo sapiens cDNA, mrNA sequence
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AW747905.1 (31:7662746
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                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
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                   121 cgagacattcataacaagaaatctcaagcttccgtcagtgatcctatgaatgcactccag 180
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                                                                   63 CTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCATTATCCATTTT 122
                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                3 ATGAGGAAAGCTGGTGTGGCACACAGTAAATCCAGCAAGGATATGGAGAGCCATGTTTTC 62
al Similarity 99. 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemannédkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALU46886 757 bp mRNA EST 29-FEB-2000 DKFZp586E2117_r1 586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586E2117 5', mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp586E2117) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
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/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1/Mlu1"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1/Mlu1"
/ 233 c 208 g 116 t 1 others
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/clone_lib="586 (synonym: hute1)"
/tissue_type="uterus"
/dev_stage="adult"
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/db_xref="taxon:9606"
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99.7%; Pred. No. 1.2e-148;
vative 0; Mismatches 1;
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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Email: asimpson@ludwig.org.br
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                                                                                /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                             tissue mRNA and cDNA amplification were
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BG122694.1 GI:12616203
EST.
                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
Plate: LLAM10235 row: k column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 956)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG122694 956 bp
602351822F1 NIH_MGC_90
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
     246
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                                                                                                                                                                                                                                                                     quality sequence stop: 611.
/tissue_type="adenocarcinoma, cell line"
/lab_host="DHIUB (phage-resistant)"
/note="organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
a 325 c 251 g 134 t
                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:4450300"
                                                                                                                                                      /clone_lib="NIH_MGC_90"
                                                                                                                                                                                                               /organism="Homo sapiens
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%; Score 340; DB 10; 100.0%; Pred. No. 2e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 30-JAN-2001 clone IMAGE:4450300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distr:bution: MGC clone distribution information can be
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                182 a
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/tissue_type="adenocarcinoma cell line"
/lah_host-"DH10B (phage-resistant)" Site_1: xhoI; Site_2:
/note="Organ: colon; Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: colon; Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: colon; Vector: pOTB7; Site_1: xhoI; Site_2: potentially clored into EcoRI/XhoI sites using the following 5;
/noted into EcoRI/XhoI sites using the following 5;
/noted into EcoRI/XhoI sites using the following 6;
/noterit GCACGAG(G) Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stiatagene) and Superscript II RT (Life Technologies)"
/note="Organ: Colon organization of the colon organization organization organization" organization organiza
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4583495"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_15"
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 Mismatches

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Qy 밁 Š B δÃ DЬ δÃ ф QΥ В γΩ Бр Matches 369; Query Match Best Local Similarity 362 AGCAGCAGGC 371 437 agcagcaggc 446 377 agctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagcagc 436 317 ggacctcggggatggcccctcacagcatggctgtcgtgtctacggcaactccacagaccc 376 197 ctgctgcgggagccgctggaattggcatgcctcctccggggcccggggacagtctctgggcg 256 137 agaaatctcaagcttccgtcagtgatcctatgaatgcactccagagcctgactggcggac 196 302 AGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGTTCCAGCAGC 361 242 GGACCTCGGGGATGGCCCCTCACAGACATGGCTGTCGTGTCTACGGCAACTCCACAGACCC 122 CTGCTGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCGGGACAGTCTCTGGGCG 181 62 AGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGAC 121 77 gggacgaatacctttctctcgtggccaggctcattatccattttcgagacattcataaca 136 Conservative 18.3%; 99.7%; 0; Mismatches Score 319; DB 11; Length 878; Pred. No. 8.9e-136; Indels Gaps

Search completed: April 30, 2002, 20:39:03 Job time: 14456 sec

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Minimum DB
Maximum DB
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Perfect score:
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seq length: 2000000000
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  Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/
2: /cgn2_6/ptodata/1/
3: /cgn2_6/ptodata/1/
4: /cgn2_6/ptodata/1/
5: /cgn2_6/ptodata/1/
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd.
  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                           DВ
US-09-043-303-7
US-09-253-991-3
US-09-253-991-3
US-08-253-110-2
US-08-253-110-2
US-09-041-886-22
US-09-041-886-22
US-09-298-441-3
US-08-779-801-5
US-08-779-801-3
US-08-779-801-3
US-08-32-766A-6
US-08-32-766A-6
US-08-458-356-150
US-09-08-458-363-13
US-09-08-697A-13
US-09-043-303-13
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US-08-469-8028-6
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4272.243 Million cell updates/sec
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                                                                                                          Sequence 7, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 22, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 150, App
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 Sequence Sequence Sequence Sequence Sequence
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Sequence
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Sequence 1,
 3, Appli
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13, Appli
12, Appli
6, Appli
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RESULT 2 US-09-253-691 ; Sequence 3, Patent NO. ; GENERAL INF APPLICANT: TITLE OF I TITLE OF I FILE REFER CURRENT AP CURRENT FI EARLIER AP EARLIER FI NUMBER OF SOFTWARE: SEQ ID NO 3 I LENGTH: 3 TYPE: DNA	Query Matc Best Local Matches Qy 664 ca Qy 661	RESULT 1 US-09-043-303-7 Sequence 7, Application US/090 patent No. 6251589 GENERAL INFORMATION: APPLICANT: TSUJI, Shoji APPLICANT: Primers 7 FILE OF INVENTION: Method fc TITLE OF INVENTION: Primers 7 FILE REFERENCE: 0760-0241P CURRENT APPLICATION NUMBER: I CURRENT FILING DATE: 1998-05 EARLIER APPLICATION NUMBER: I CURRENT FILING DATE: 1996-07 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7 LENGTH: 203 TYPE: DNA ORGANISM: p-2093 plasmid US-09-043-303-7		22 22 23 23 23 23 24 24 24 24 24 24 24 24 24 24 24 24 24
2 3-691-3 3-691-3 3-691-3 3-691-3 3-691-3 3-691-3 3-691-3 4-6124100 4-612410	atch Sal Simi 45; caacagc	1 3-303-7 ice 7, Ap ice 7,		W W W W W W W W W W W W W W W W W W W
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JIN Diagno: Diagno: Using (Using (2/36) (INMBER (INMBE	y 100 rvative cagcago	on US/( atujirc atujirc method primer; 0241p-024p-024p-024p-024p-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0		165 168 168 171 171 171 195 195 234 234 330 325 477 506 688 715 508
092 Tri 12: U 02- 02- Win	69; agc	090 0 0 05- 07-		412121212424124428
53691 c Method and Kit for nucleotide Repeats Se 5/09/253,691 29 28 8 98-6,278 dows	2.6%; Score 45; DB 4; Length 2 100.0%; Pred. No. 2.1e-11; tive 0; Mismatches 0; Indel cagcagcagcagcagcagcagcagcag 708 	/09043303  ro d for Diagnosing Spinocerebellar rs Therefor R: US/09/043,303 -05-18 R: PCT/JP96/01999 -07-18	ALIGNMENTS	US-09-043-303-17 US-08-469-802B-4 US-08-267-803B-5 US-08-469-802B-5 US-08-267-803B-5 US-08-267-803B-2 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-3 US-08-267-803B-7 US-08-813-927B-3 US-09-135-994-1 US-08-469-802B-7 US-08-267-803B-7 US-08-267-803B-7 US-08-268-803B-7 US-08-268-803B-7 US-08-98-416-915 US-08-998-416-515 US-08-998-416-590 US-08-998-416-590 US-08-998-416-590 US-08-998-416-590 US-08-998-818-727-2 US-09-205-680A-2
Neuropsychiatric Diseases guence	203; els 0; Gaps 0 8	ar Alaxia Type 2 and		Sequence 17, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 915, App Sequence 915, App Sequence 590, App Sequence 2, Appli

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RESULT

→ ; Sequence 12, Application US/09041886
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                                       US-09-041-886-12
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08531927B Patent No. 5840491
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APPLICANT: Kakizuka,
TITLE OF INVENTION: 1
Patent No. 5840491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Granahan, Patricia
REGISTRATION NUMBIR: 32,227
REFERENCE/DOCKET HUMBER: AFI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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MEDIUM TYPE: FIGHT

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

ENTITY OF THE PROPERTY O
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LENGTH: 1776 base pair
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDR:2SS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                               667 cagcaacagcagcagcagcagcagcagcagcagcag 708
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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CITY: Lexington
STATE: Massachu
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21-SEP-1994
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N: 435
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100.0%; Pred. No. 4.8e-10;
ative 0; Mismatches 0;
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US-08-553-110-2
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Patent No. 5723301
GENERAL INFORMATION:
APPLICANT: Burke, James R.
APPLICANT: Vance, Jeffrey M.
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
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TOPOLOGY: lin
MOLECULE TYPE:
FEATURE:
                                                                                                                                                       APPLICANT: Vance, Jeffrey M.
APPLICANT: Enghild, Jan
APPLICANT: Strittmatter, Warren J.
TITLE OF INVENTION: Therapeutics for Diseases Associated
TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STREET: 43/
CITY: San Diego
STATE: California
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT IMPORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
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CURRENT APPLICATION DATA
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APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                     921 CAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
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                                                                                                   STREET: P.O. Dr
CITY: Charlotte
                                                               COUNTRY:
                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 2.4%; Score 42; DB 4; Local Similarity 100.0%; Pred. No. 4.8e-1 es 42; Conservative 0; Mismatches
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                                             28234
                                                                               No. 5723301th Carolina
                                                                                                                     P.O. Drawer 34009
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                                                               United States of America
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                                                                                                                                          Kenneth D. Sibley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent NO. JACKET OF INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09041886 Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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                                                                                             TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8049
INFORMATION FOR EGO ID NO: 22
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 54(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPHONE: 919-40-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216 CAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                   LENGTH: 4279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1853 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States
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SYSTEM: PC-DOS/MS-DOS
                      linear
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DNA (genomic)
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100.0%; Pred. No.
ative 0; Mismatcl
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; NAME/KEY: gene
; LOCATION: (0)...(0)
; OTHER INFORMATION: Achoaete scute homologous protein (ASH1) gene;
; OTHER INFORMATION: Genbank accession L08424
US-09-234-332-4
                                                                                                                                                                                                                                            Sequence 20, Application US/09041886
Patent NO. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
UMMBER OF SEQUENCES: 72
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; Patent No. 6087168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%; Score 38; DB 3; I Best Local Similarity 100.0%; Pred. No. 3.2e-08; Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cedars-Sinai Medical Center APPLICANT: Michel F. Levesque, M.D. APPLICANT: Toomas Neuman, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO TITLE OF INVENTION: HEURONS; TRANSDIFFERNTIATION OF EPIDERMAL CELLS FILE REFERENCE: PO7 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Human
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                         COUNTRY: U
                                                                                                                                           CITY: San Diego
STATE: California
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                                                                                                                                                                                    E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                        United States
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239..3794

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 9
US-08-779-801-5
; Sequence 5, Application US/08779801
; Patent No. 5853995
; Patent No. 5853995
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; LOCATION:
US-09-041-886-20
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Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0;
                       NAME: Benjamin Agron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ II NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3596
TYPED: 3596
TYPED: NO: 14.5 2514
                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBEF:
EILING DATE:
ATTORNEW ATTE
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FCRM:
MEDIUM TYPE: Florpy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft word for Macintosh
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                            ATTORNEY/AGENT INFOFMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Benjamin
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TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERAL INFORMATION:
APPLICANT: Lee, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Campbell, (athryn A. REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET HUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 80:
CITY: Houst
STATE: Text
COUNTRY: US
ZIP: 77071
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                            : Houston
E: Texas
TRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Benjamin Aaron Adler, Ph.D., J.D.
8011 Cancle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
3..3550
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RESULT 10
US-09-298-441-5
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09298441 Patent No. 6303307 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 2.2%; Score 38; Lb. Best Local Similarity 100.0%; Pred. No. 3.2.
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ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: brain
IMMEDIATE SOURCE:
LIBRARY: primary human brain cDNA
CLONE: BI-1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
MOLECULE TYPE:
DESCRIPTION: of
HYPOTHETICAL: no
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
SOFTWARE: MICROSOft Word for Macintosh
APPLICATION NUMBER: US/09/298,441
                             DESCRIPTION:
HYPOTHETICAL:
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type 6
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESS: 5 ADDRESS: 5
ORIGINAL SOURCE:
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3596 basepairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 8011 (CITY: Houston STATE: Texas
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 77071
                                                                                                                                                                                                                                      nucleic acid
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8011 Candle Lane
                                                                                                                                                                                                                                                                       3596 basepairs
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                                                                                                                                                                                                        double-stranded
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; Pred. No. 3.2e-08
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ORGANISM:

human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.2%; Score 38; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 3:
                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: primary human brain cDNA CLONE: BI-1(V2)-GGCAG POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2970 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGC 3007
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: prima
CLONE: BI-1(V2
                                                                                                                                                    DESCRIPTION: cl
HYPOTHETICAL: no
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 00-
STREET: 00-
TTTY: Houston
                                   IMMEDIATE SOURCE:
LIBRARY: prima:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 cagcagcagcagcagcagcagcagcagcagcagcaggc 710
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHROMOSOME/SEGMENT: 19p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Benjamin Aaron Adler, Ph.D., REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/779,801 FILING DATE: January 7, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                    nucleic acid
                  : primary human
BI-1-GGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Benjamin Aaron Adler, Ph.D., J.D. 8011 Candle Lane
                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 7, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain
                                                                            brain
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                                                                                                                                                                                                                                                        double-stranded
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US-09-298-441-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.2%; Score 38; DB 2; Best Local Similarity 100.0%; Pred. No. 3.2e-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3632 basepairs
                                                              ORGANISM: human
TISSUE TYPE: br
IMMEDIATE SOURCE:
LIBRARY: primar
                                                                                                                                                      DESCRIPTION:
HYPOTHETICAL: r
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-0321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
TITLE OF INVENTION: and a Diagnostic Test for Spinocerebellar Ataxia Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3006 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCC 3043
                                POSITION IN GENOME:
                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 cagcagcagcagcagcagcagcagcagcagcagcagc
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                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
              CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Conservative
                                                                                                                                                                                                                                                          nucleic acid
                                                 : primary human brain cDNA BI-1-GGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                      human
                                                                                                                                                         no
                                                                                                                                                                                                                       linear
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                                                                                                                                                                                          CDNA
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              19p13
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 Mismatches

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Query Match
Best Local Similarity

Matches

38; Conservative

2.2%; Score 38; DB 4; I 100.0%; Pred. No. 3.2e-08; ative 0; Mismatches 0;

Length 3632; 8; 0; Indels

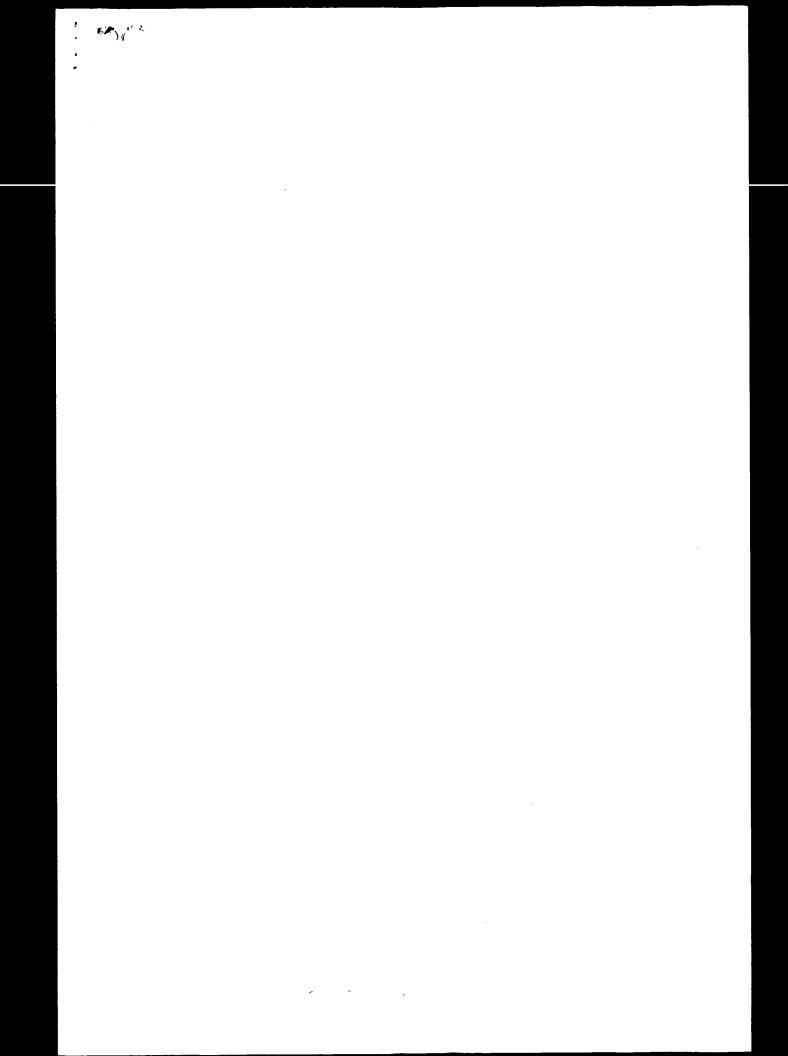
0;

Gaps

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) Db
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APPLICATION NUMBER: US/07/581
FILING DATE: 12-S:P-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
APPLICATION NUMBER: 746,520
FILING DATE: 05-J(IL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-J(IN-1985)
APPLICATION NUMBER: 627,811
FILING DATE: 05-J(IL-1984)
SEQ ID NO:10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
5273901-10
;Patent No. 5273901
;Patent No. 5273901
;Patent No. 5273901
;SUSAN D.;POPE, SHAKON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;SUSAN D.;POPE, SHAKON H.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, MICHAEL D.;
;NUMBER OF SEQUENCES 11
                                                               QΥ
                                                                                                                                                                                                                          5482709-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON, SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.; AUGISTINE, PATRICIA C.;DANFORTH, HARRY D.

TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH ELICITS ANTIBODIES AGAIN:ST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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5482709-9
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                                                                                                                                                                                                                                                                         SEQ ID NO:9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Patent No. 5482709
                                                                                                               Matches
                                                                                                                                                       Query Match
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FILING DATE: 08-NCV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
ADDITION NUMBER: 1501
             181 cagcagcagcagcagcagcagcagcagcagg 217
                                          673 cagcagcagcagcagcagcagcagcagcagcagg 709
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                                                                                                               Local Similarity hes 37; Conserv
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
                                                                                                                                                                                                                                                       LENGTH: 228
                                                                                                                                                                                                                                                                                                    FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 2.1%; Score 37; DB 6; I
Local Similarity 100.0%; Pred. No. 9.2e-08;
les 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 228
                                                                                                          2.1%; Score 37; DB 6; I ilarity 100.0%; Pred. No. 9.2e-08; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/148,432
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                                                                                                                                                       Length 228;
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                                                                                                               Indels
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                                                                                                     Gaps
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                                                                                                          0;
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Search completed: April 30, 2002, 20:40:57 Job time: 10655 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 6, Application US/08332766A
; Patent No. 5843647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-332-766A-6
                                                                                                                                                                                          Ouery Match 2.1%; Score 37; DB 2; L1
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 286 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: JEFFREYS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JEFFREYS, Alectory applicant: ARMOUR, John TITLE OF INVENTION: SIMPL NUMBER OF SEQUENCES: 125 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING CALL
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9326052.9
APPLICATION NUMBER: GB 9326052.9
APPLICATION 2 21 DEC 1993
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BIRD DONALD J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          187 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 223
                                                                                                                              673 cagcagcagcagcagcagcagcagcagcagcagg 709
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 01-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217211/M94/0434/GB
                                                                                                                                                                                                                                    Length 286;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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                                                     US-09-668-119-1
1740
1 atgaggaaagctggtgtggc.....cacattcgttccagccatga 1740
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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12	11	10	9	8	7	6	G	4	w	2	1	No.	Result	
524.4	526.8	527	530	536.6	572.8	615.2	650.8	655	662	697.6	722.8	Score		
30.1	30.3	30.3	30.5	30.8	32.9	35.4	37.4	37.6	38.0	40.1	41.5	Match	Query	æ
526	656	914	1019	723	939	620	757	886	2752	730	776	Match Length DB		
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BE019568	BE390284	BG468341	BG335275	BE279307	BG336790	BE384305	AL046886	BG281923	BC005027	BG766214	BG750043	ID		
BE019568 ba83f05.y	BE390284 601285167			BE279307 601157640	BG336790 602405533	BE384305 601272684		~	BC005027 Homo sapi	BG766214 602737942	BG750043 602708813	Description		

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BF14390 AW501171 BE889171 BF922390 BG686794	AI787536 BF600990 N49344 AA93166 BI011820 BG982938	BE251464 AW227792 BG982761 BG982754 BI015868	BE163519 BI024741 BE284329 BG281322 BG471322 AW747905	BG338685 BG122694 BG17319 BC003221 BG386117 BG386117	BG746380 AA664125 BE410770 BE391135 AW603679
60178643 UI-HF-BP 60151343 QV2-NT01 60265076	AI787536 ul19el1.y BF600990 265840 MA N49344 yy23el0.rl AA982166 ua21h02.r BI011820 PM1-EN006 BG989938 BM0-CN015	BE251464 601109346 BE251464 601109346 AW227792 up14c09 y BG982761 PMO-CN015 BG982764 PMO-CN015 BG1015868 PMO-ET025	BE163519 QV3-HT046 BI024741 PM0-MT020 BE284329 601087443 BG421322 602451441 AW747905 QV1-BN000 BI080323 60285328	BG338685 602436442 BG122694 602351822 BG177319 602313922 BC003221 Mus muscu BG386117 602455292 BG915202 602814508	0

## ALIGNMENTS

FEATURES SOUTCE	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG750043 LOCUS DEFINITION
	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	Primates;	B6/50043.1 GI:14060696 EST. human. Homo sapiens Howo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	BG750043 776 bp mrNA EST 15-MAY-2001 602708813F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845411 5', mrNA sequence.

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LOCUS BG766214 730 bp mRNA EST 15-MAY-2001 bgFINITION 602737942F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4862938 5',
                                                             BG766214
                                                                                     RESULT
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                                                                                                                                                                                                                                                                          661 GGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGTCT-CCCATGCTGTC 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 gcagcagcagcatctaattaaattgcatcatcaaaattcagcaacagatacagcagca 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGCGGCGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGCTCAGCAGAG 120
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1163 cgtccccgcagcccagcccagctcacagcccaactccaacgtcagctctggccctg 1222
                                                                                                   1103 cctcgccgtcaccgggccagcaggtgcagaccccgcagtcgatgccccctcccccccagc 1162
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                                                                803 atcacacacagcaccaccagccgccaccagccccagcagcctccagttgctcagaacc 862
                                                                                                                                                                                                                                                                                                                                                                                  983
                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              923 tccctggacaaatgttgtatacccaaccaccactgaaatttgtccgagctccgatggtgg 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 aaccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcgcaagctc 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTC 121
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                                                                                                                                                                                                                                                                                                                                                  AGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCCATGCTGT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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/lab_host="DBIOB (phage resistant)"
/note="organ: skin; Vector: poTB7; Site_1: XhoI; Site_2:
/note="organ: skin; Vector: poTB7; Site_1: XhoI; Site_2:
/note="organ: skin; Vector: poTB7; Site_1: XhoI; Site_2:
/note="organ: skin; Vector: poTB7; Site_1: XhoI; Site_2: Sing the following 5 adaptor:
/note Scorn/XhoI sites using the following 5 adaptor:
/note Scorn/XhoI sites using the following 5 adaptor:
/note Scorn/XhoI sites using the following in the laboratory
/note Scorn/XhoI sites skin (Intradene) and Superscript
/note Scorn/XhoI synthesis kit (Stratagene) and Superscript
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Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_49"
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                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov Series: IRAL Plate: 18 Row: a Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7209306
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. COT DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Submitted (26-MAR-2001) National Institutes of Health, Mammalian Submitted (26-MAR-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer 
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mRNA sequence.
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                         BG281923 886 bp
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/note="Vector: pOTB7"
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/clone_lib="NIH_MGC_7"
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Pred. No. 1.2e-99;
                         Homo sapiens cDNA clone IMAGE: 4545433 5',
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707 aggetttggaggeenageeaceaatteag-eageeacegatgeageageeacageeteeg 765
                                                                                  651 gctgcagctccaacaacagcagcagcagcagcagcagcagc----agcagcagcagc 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 ogtgtctacggcaa:stccacagacccagctgcagctccagcaggtggcgctgcagcagca 410
                                                        302 GCATCATCAAAATCAGCAACAGATACAGCAGCAGCAGCAGCAGCGGAATAGCACA 361
                                                                                                                                                                                    591 gcatcatcaaaatcagcaacagatacagcagcagcaacagcagctgcagcgaatagcaca 650
                                                                                                                                                                                                                                                              242 AGTGCAGCAGCAGCIGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATT 301
                                                                                                                                                                                                                                                                                           182 GCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGT 241
                                                                                                                                                                                                                                                                                                                                                                                                471 gcagcaacagcagcagttccaaggctcagcagagtgccatgcagcagcagttccaagcagt 530
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es 749; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Librar/ Preparation: Ling Hong/Rubin Laboratory cDNA Librar/ Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM1230 row: g column: 02 High quality sequence.stop: 876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
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/db_xraf="taxxx:5006"
/db_xraf="taxxx:5006"
/cl.ne="TMAGE:4545433"
/cl.ne=lib="NHIMGC_20"
/tissue_type="melanotic melanoma"
/la.host="DH10B (phage-resistant)"
/la.host="DH10B (phage-resistant)"
/la.host="DH10B (phage-resistant)"
/la.host="DH10B (phage-resistant)"
/la.host="DH10B (phage-resistant)"
/noce="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/coal; cDNA made by oligo-dT priming. Directionally
clored into EcoRJ/XhoI sites using the following 5;
ada_stor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
34 a 299 c 231 g 122 t
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93.7%;
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                                                                                                                                                                                                                                                                                                                                                                                               This is the 5' sequence of the clone insert Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer Clone from (DKFZ); Email s. wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 757)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Essential (Koehrer, et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL046886 757 bp mRNA EST 29-FEB-2000 DKFZp586E2117_r1586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586E2117 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                     This clone (DKFZp586E2117) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                               Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                   No s1 sequence available
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                     199 a
                                                                                  /Clone="DKFZp586E2117"
/Clone=lib="586 (synonym: hutel)"
/tissue_type="uterus"
/tev_stage="adult"
             /lab_host="DH10B"
/note="Vector: pSpc
/note="233 c 208 g
                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                         ocation/Qualifiers
                                      pSport1; Site_1: NotI; Site_2: SalI/MluI"
                     1 others
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Query Match

Best Local Similarity

37.4%; 98.0%;

Score 650.8; DB : Pred. No. 8.2e-98

DB 10; Length 757

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RESULT 6
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                          JOURNAL
                                                  AUTHORS
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Unpublished (1999)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 620)
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National Institutes of Health, N
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: DOTB7; Site_1: XhoI; Site_2: Xising the following 5;
/note into EcoRI/XhoI sites using the following in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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/clone="IMAGE:3613868"
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Tissue Procurement: ATCC
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602405533F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542993 5'
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 939)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="NHL_MGC_21"
/fissue_type="Choriocarcinoma"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LICM179 row: o column: 09
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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          177 a
/tissue_type="choriocarcinoma"
//Lab_host="DH108 (phage-resistant)"
//Lab_host="DH108 (phage-resistant)"
//note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
//note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
//note="organ: placenta; Vector: poTB7; Site_susing the potentially cloned into Ecoal/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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                      CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 23
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602403789F1 NIH_MGC_21 Homo
                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                       Unpublished (1999)
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                                                                           CGATGGTGCTGCAGCAGCACCCAGTG-AGCCCCAGGTGCAGC
                                                                                                                                     CGCAAGCTCTCCCTTGACAAATGTAGTATACCCAA-CACCACTGAAATTTGTCCGAGCTC
                                                                                                                                                                                                     CTCAGAACCAATCACAACTCCCGCAACAGTCGCAGA-CCAGCCTTTGGTGTCACAGG
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
98 a 325 c 238 g 157 t 1 others
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4541110"
/clone_lib="NIH_MGC_21"
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Pred. No. 6.3e-78;
0; Mismatches 10;
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DEFINITION

mRNA

sequence.

BG468341 914 bp mRNA 602509947F1 NIH\_MGC\_15 Homo sapiens

CDNA

clone

IMAGE: 4644299

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1503 gagccttctggaca:tctgacagacccctcgaagcggtgtcccctgaagaccttgcaaaa 1562
                                                                                                                                                                                                                                                                    1443 ccgcatgatcaaca.agatcgacaagaacgaagacagaaaaaaggacctgagtaagatgaa 1502
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                                                                                                                    303 GAGCCTTCTGGACACTTCTGACAGACCCCTCGAAGCCGTTGCCCCTGAAGACCTTGCAAAA 362
                                                                                                                                                                                                                                      243 CCGCATGATCAACA.\GATCGACAAGAACGAAGACAGAAAAAAAGGACCTGAGTAAGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GCCCTCCCAGAGCCCAGTGACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CAACGTCAGCTCTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image llnl.gov
Plate: LLCM145 row: n column: 12
High quality sequence stop: 812.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BG468341.1 GI:13400611
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 :0 914)
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/lal_host="DH10B (phage resistant)" Site_1: xhoI; Site_2:
/no:e="organ: colon; Vector: pOTB7; Site_1: xhoI; Site_2: xhoI]
/localine into EcoRI/XhoI sites using the following 5;
/no:ed into EcoRI/XhoI sites using the following 5;
/no:ed into EcoRI/XhoI sites using the following 5;
/no:ed into EcoRI/XhoI sites using the following 6;
/no:ed into EcoRI/XhoI sites using following 6;
/no:ed into EcoRI/XhoI sites using following for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. RuDin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
/no:ed into EcoRI/XhoI sites using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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/db_xref="taxon:9606"
/clone="IMAGE:4644299"
/clone_lib="NIH_MGC_15"
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 Mismatches

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Pred. No. 2e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                  598 caaaatcagcaacagatacagcagcagcagcagcagctgcagcgaatagcacagctgcag 657
                                                                                                                                                                                                                                                                                                         538 cagcagcagcagcagcagcagcagcagcagcagcagcatctaattaaattgcatcat 597
718 gcccagccaccaattcagcagccaccgatgcagcagccacagcctccgccctcccaggct 777
                                                           483 CAACATCCGCTCACCTGTCTTCAACCATTCCCTGTACCGCACATTCGTTCCAGCCATGA 541
                                                                                                                                                                                                                                                                                1 CAGCGGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAAGTGCATCAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                       CAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih
Tissue Procurement: ATCC
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Plate: LLCM257 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 656)
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/clone_lib="NIH_MCC_44"
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ECORI; CDNA made by Oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using XAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/db_xref="taxon:9606"
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National Institutes of Health, M
Unpublished (1999)
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Site_2: EcoRI; cDNA made by oligh-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by
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the laboratory of Gerald M.
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BG746380
BG746380.1 GI:
                                                                                                                                      Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM1708 row: p column: 12
                                                                                                                                                                                                      Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1454 acaagatcgacaag1acgaagacagaaaaaaggacctgagtaagatgaagagccttctgg 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1274 gcccagtgacggcgggaccccacagaacttcagtgtcccctcacctggacctttaaaca 1333
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                                                                                                                                                                                                                                                                                                                                                                                             429 CGACCAAACAGCAGTACCTATGCCAGCCGCTCCTGGATGCCCGTCCTGGCCAACATCCGCT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 GCCCAGTGACGGCGGGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAAACA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CAGGCCCAGCCCCA CTCCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCCTCCCAGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccctggagaaactclagaatgacat-gcggtgcccactcccccaccgcccccggtgccac 1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acattctgacagaccctcgaagcggtgtcccctgaagaccttgcaaaagtgtgagatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTGGAGAAACTC AAGAATGACATGGCGGTGCCCACTCCCCCACCGCCCCCGGTGCCAC
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                                                                     Homo sapiens
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/db_xxef="taxon:9606"
/db_xxef="taxon:9606"
/clone="INAGE:,4857083"
/clone="INAGE:,4857083"
/clone="Ilb="NIH_MGC_15"
/fissue_type="adenocarcinoma cell line"
/fiscoll collowing 5/
ada,tor: GCACGAG(G) size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(St:atagene) and Superscript II RT (Life Technologies)"
// 3 a 264 c 186 g 126 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512.8; DB 11; Length 756; Pred. No. 4.2e-75;
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                                                           848 cagttgctcagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgt 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 tccagcagcagcagcagcggcgctacagcagcagcagcagcagcagcagcaacagcagcagt 487
                                      62
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                                                                                                                                                 CAATTCAGCAGCCACCGATGCAGCCACCACCACCCTCCCCAGGCTCTGCCCCAGC 123
                                                                                                                                                                                                                                                        caattcagcagccaccgatgcagccaccagcctccgccctcccaggctctgccccagc 787
                                                                                                                                                                                                                                                                                                       AGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCAGCCTTTGCAGGCCCAGCCAC 183
                                                                                                                                                                                                                                                                                                                                                   aacagatacagcagcagcaacagcagctgcagcgaatagcacagctgcagctccaacaac 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tccaggctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagc 547
                                      CAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGT
                                                                                                                            AACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarriini; Hominidae; Homo.

1 (bases 1 to 482)

1 (bases 1 to 482)

1 (liler,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Stratagene lung (#937210)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:855654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Louis, MO 63108
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63

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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                        Matches 496;
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876 cccgccacagtcgcagacccagcctttggtgtcacaggcgcaagctctccctggacaaat 935
                                                                                                                                 524 GCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCA
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                                                                                                                     404
                                                                                                                                                                                       464 GCAGCAGCAGCATTTGCAGGCCCAGCCAATTCAGCAGCCACCGATGCAGCAGCC 405
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                                                             gcagcagcaggctttggaggcccagccaattcagcagccaccgatgcagcagcc 755
                                                                                                                                                                                                                                                                                  gcagcgaatagcacagctgcagctccaacaacagcaacagcagcagcagcagcagcagca
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                                        CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution infocusion distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM333 row: b column: 22 High quality sequence start: 48 High quality sequence stop: 522. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 524)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE_3636021"
/clone_lib="NIH_MGC_21"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="Pull0B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Sites using the following 5' adaptor: GGCACAGG(G). Sizes using the following 5' adaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong In the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     27.0%;
94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 bp
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                     Score 469.4;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                    5.7e-68;
ches 26;
                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                         Length 524;
                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                             224 GTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCAC
                                                                                                                                                                                          936
                                                                                                                                                                                                                     284
                                                                 tggtggctcccggagtccaggtcagccagagcagcctccccatgctgttctctcgccgtcac 1114
                                                                                                                        GCGGGCCACGCAGGCACAGACCCTAACCAGCTCAAGTGCCCCC
                        cgggccagcaggtgcagaccccgcagtcgatgccccctccccc 1157
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                                                                                                        CAGTGCAGCCCCAGGTGCAGCAGCAGCAGACAGCAGACAGCTCAGGCTGCCCAGA
                                                                                                                                                                                                                   gttgtatacccaaccaccactgaaatttgtccgagctccgatggtggtgcagcagccc-c
                                                     45
                                                                                                        105
                                                                                                                                                              165
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Search completed: February 28, 2002, 18:34:06 Job time: 8439 sec